

Database : UniProt\_02:\*

1: uniprot\_sprot:\*

2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result	Query					Description
No.	Score	Match	Length	DB	ID	
1	2680	100.0	507	2	Q9NQH7	Q9nqh7 homo sapien
2	2680	100.0	507	2	CAG30328	Cag30328 homo sapien
3	2676	99.9	507	2	Q6I9V9	Q6i9v9 homo sapien
4	2676	99.9	507	2	Q9BV27	Q9bv27 homo sapien
5	2676	99.9	507	2	CAG33677	Cag33677 homo sapien
6	2255	84.1	428	2	Q8NDA6	Q8nda6 homo sapien
7	1833	68.4	502	2	Q6DD23	Q6dd23 xenopus lae
8	1706.5	63.7	386	2	Q8BHT9	Q8bht9 mus musculu
9	1487	55.5	510	2	Q6NYT0	Q6nyt0 brachydanio
10	1487	55.5	510	2	AAH66473	Aah66473 brachydan
11	1393	52.0	278	2	Q9BVH0	Q9bvh0 homo sapien
12	895.5	33.4	513	2	Q7Q4S9	Q7q4s9 anopheles g
13	895	33.4	480	2	Q8GYQ0	Q8gyq0 arabidopsis
14	862	32.2	545	2	Q9W5W7	Q9w5w7 drosophila
15	821.5	30.7	451	2	Q9ZPZ5	Q9zpz5 arabidopsis

3 to lab  
date

RESULT 1

Q9NQH7

ID Q9NQH7 PRELIMINARY; PRT; 507 AA.  
AC Q9NQH7;  
DT 01-OCT-2000 (TrEMBLrel. 15, Created)  
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)  
DT 01-OCT-2004 (TrEMBLrel. 28, Last annotation update)  
DE Hypothetical protein LOC63929 (DJ1057D18.1 protein).  
GN Name=LOC63929; Synonyms=dJ1057D18.1;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Collins J.E., Huckle E.J.;  
RL Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.  
RN [2]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Lung;  
RX MEDLINE=22388257; PubMed=12477932;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,  
RA Jones S.J., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
RT and mouse cDNA sequences.";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
RN [3]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Lung;  
RA Strausberg R.;  
RL Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.  
RN [4]  
RP SEQUENCE FROM N.A.  
RA Collins J.E., Wright C.L., Edwards C.A., Davis M.P., Grinham J.A.,  
RA Cole C.G., Goward M.E., Aguado B., Mallya M., Mokrab Y., Huckle E.J.,  
RA Beare D.M., Dunham I.;  
RL Submitted (MAY-2004) to the EMBL/GenBank/DDBJ databases.  
DR EMBL; AL365514; CAB97210.1; -.  
DR EMBL; BC004989; AAH04989.1; -.  
DR EMBL; CR456442; CAG30328.1; -.  
DR HSSP; P15034; 1A16.  
DR MEROPS; M24.026; -.

DR GO; GO:0008235; F:metalloexopeptidase activity; IEA.  
 DR GO; GO:0008233; F:peptidase activity; IEA.  
 DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.  
 DR InterPro; IPR000994; Peptidase\_M24.  
 DR InterPro; IPR007865; Pept\_M24B\_N.  
 DR Pfam; PF05195; AMP\_N; 1.  
 DR Pfam; PF00557; Peptidase\_M24; 1.  
 KW Hydrolase; Hypothetical protein.  
 SQ SEQUENCE 507 AA; 57033 MW; 82D886736ABD0B5B CRC64;

Query Match 100.0%; Score 2680; DB 2; Length 507;  
 Best Local Similarity 100.0%; Pred. No. 1.e-192;  
 Matches 507; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1 MPWLLSAPKLVPAVANVRGLSGCMLCSQRRLSQQVPERIPNRYLGQPSFTPHPHLLRP	60
Db	1 MPWLLSAPKLVPAVANVRGLSGCMLCSQRRLSQQVPERIPNRYLGQPSFTPHPHLLRP	60

Qy	61 GEVTPGLSQVEYALRRHKLMSLIQKEAQGQSGTDQTVVVLSNPTYYMSNDIPYTFHQDNN	120
Db	61 GEVTPGLSQVEYALRRHKLMSLIQKEAQGQSGTDQTVVVLSNPTYYMSNDIPYTFHQDNN	120

Qy	121 FLYLCGFQEPDSILVLQSLPGKQLPSHKAILFVPRRDPSRELWDGPRSGTDGAIALTGVD	180
Db	121 FLYLCGFQEPDSILVLQSLPGKQLPSHKAILFVPRRDPSRELWDGPRSGTDGAIALTGVD	180

Qy	181 EAYTLEEFQHLLPKMKAETNMVWYDWMRPSHAQLHSDYMQPLTEAKAKSKNKVRGVQQLI	240
Db	181 EAYTLEEFQHLLPKMKAETNMVWYDWMRPSHAQLHSDYMQPLTEAKAKSKNKVRGVQQLI	240

Qy	241 QRLRLIKSPAIEIERNQIAGKLTSQAFIETMFTSKAPVEEAFLYAKFEFECRARGADILAY	300
Db	241 QRLRLIKSPAIEIERNQIAGKLTSQAFIETMFTSKAPVEEAFLYAKFEFECRARGADILAY	300

Qy	301 PPVVAGGNRSNTLHYVKNNQLIKDGEVLLDGGCESSCYVSDITRTWPVNGRFTAPQAE	360
Db	301 PPVVAGGNRSNTLHYVKNNQLIKDGEVLLDGGCESSCYVSDITRTWPVNGRFTAPQAE	360

Qy	361 YEAVLEIQRDCLALCFPGTSLENIYSMMLTLIGQKLKDLGIMKNIKENNAFKAARKYCPH	420
Db	361 YEAVLEIQRDCLALCFPGTSLENIYSMMLTLIGQKLKDLGIMKNIKENNAFKAARKYCPH	420

Qy	421 HVGHYLGMDVHDTDPMPRSPLQLQPGMVITIEPGIYIPEDDKDAPEKFRGLGVRIEDDV	480
Db	421 HVGHYLGMDVHDTDPMPRSPLQLQPGMVITIEPGIYIPEDDKDAPEKFRGLGVRIEDDV	480

Qy	481 TQDSPLILSADCPKEMNDIEQICSQAS	507
Db	481 TQDSPLILSADCPKEMNDIEQICSQAS	507

RESULT 2

## RESULT 2

CAG30328

ID CAG30328 PRELIMINARY; PRT; 507 AA.  
 AC CAG30328;  
 DT 01-JUN-2004 (TrEMBLrel. 27, Created)  
 DT 01-JUN-2004 (TrEMBLrel. 27, Last sequence update)  
 DT 01-JUN-2004 (TrEMBLrel. 27, Last annotation update)  
 DE DJ1057D18.1 protein.  
 GN DJ1057D18.1.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Collins J.E., Wright C.L., Edwards C.A., Davis M.P., Grinham J.A.,  
 RA Cole C.G., Goward M.E., Aguado B., Mallya M., Mokrab Y., Huckle E.J.,  
 RA Beare D.M., Dunham I.;  
 RL Submitted (MAY-2004) to the EMBL/GenBank/DDBJ databases.  
 DR EMBL; CR456442; CAG30328.1; -.  
 SQ SEQUENCE 507 AA; 57033 MW; 82D886736ABD0B5B CRC64;

Query Match 100.0%; Score 2680; DB 2; Length 507;  
 Best Local Similarity 100.0%; Pred. No. 1.1e-192;  
 Matches 507; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPWLLSAPKLVPAVANVRGLSGCMLCSQRRLSQQPVPERRIPNRYLGQPSFTPHPLL 60  
 |||||||  
 Db 1 MPWLLSAPKLVPAVANVRGLSGCMLCSQRRLSQQPVPERRIPNRYLGQPSFTPHPLL 60  
  
 QY 61 GEVTPGLSQVEYALRRHKLMSLIQKEAQGQSGTDQTVVLSNPTYYMSNDIPYTFHQ 120  
 |||||||  
 Db 61 GEVTPGLSQVEYALRRHKLMSLIQKEAQGQSGTDQTVVLSNPTYYMSNDIPYTFHQ 120  
  
 QY 121 FLYLCGFQEPDSILVLQSLPGKQLPSHKAILFVPRRDPSRELWDGPRSGTDGAIALTG 180  
 |||||||  
 Db 121 FLYLCGFQEPDSILVLQSLPGKQLPSHKAILFVPRRDPSRELWDGPRSGTDGAIALTG 180  
  
 QY 181 EAYTLEEFQHLLPKMKAETNMVWYDWMRPSHAQLHSDYMQPLTEAKAKSKNKGVRGVQ 240  
 |||||||  
 Db 181 EAYTLEEFQHLLPKMKAETNMVWYDWMRPSHAQLHSDYMQPLTEAKAKSKNKGVRGVQ 240  
  
 QY 241 QRLRLIKSPAIEIRMQIAGKLTSQLAFIETMFTSKAPVVEAFLYAKFEFECRARGADIL 300  
 |||||||  
 Db 241 QRLRLIKSPAIEIRMQIAGKLTSQLAFIETMFTSKAPVVEAFLYAKFEFECRARGADIL 300  
  
 QY 301 PPVVAGGNRSNTLHYVKNNQLIKDGEVLLDGGCESSCYVSDITRTWPVNGRFTAPQ 360  
 |||||||  
 Db 301 PPVVAGGNRSNTLHYVKNNQLIKDGEVLLDGGCESSCYVSDITRTWPVNGRFTAPQ 360  
  
 QY 361 YEAVLEIQRDCLALCFPGTSLENIYSMMLTLIGQKLKDLGIMKNIKENNAFKAA 420  
 |||||||  
 Db 361 YEAVLEIQRDCLALCFPGTSLENIYSMMLTLIGQKLKDLGIMKNIKENNAFKAA 420  
  
 QY 421 HVGHYLGMDVHDTPDMPRSPLQLQPGMVITIEPGIYIPEDDKDAPEKFRGLGVRIEDDV 480  
 |||||||  
 Db 421 HVGHYLGMDVHDTPDMPRSPLQLQPGMVITIEPGIYIPEDDKDAPEKFRGLGVRIEDDV 480

Qy 481 TQDSPLILSADCPKEMNDIEQICSQAS 507  
Db 481 TQDSPLILSADCPKEMNDIEQICSQAS 507

## RESULT 3

Q6I9V9

ID Q6I9V9 PRELIMINARY; PRT; 507 AA.  
 AC Q6I9V9;  
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
 DE LOC63929 protein.  
 GN Name=LOC63929;  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Ebert L., Schick M., Neubert P., Schatten R., Henze S., Korn B.;  
 RL Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.  
 DR EMBL; CR457396; CAG33677.1; -.  
 DR InterPro; IPR000994; Peptidase\_M24.  
 DR InterPro; IPR007865; Pept\_M24B\_N.  
 DR Pfam; PF05195; AMP\_N; 1.  
 DR Pfam; PF00557; Peptidase\_M24; 1.  
 KW Hydrolase.  
 SQ SEQUENCE 507 AA; 57005 MW; CFA7DDA951AEA9DC CRC64;

Query Match 99.9%; Score 2676; DB 2; Length 507;  
 Best Local Similarity 99.8%; Pred. No. 2.2e-192;  
 Matches 506; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MPWLLSAPKLVPAVANVRGLSGCMLCSQRRLSQQPVPERIPNRYLGQSPFTHPHLLRP 60  
 |||||||  
 Db 1 MPWLLSAPKLVPAVANVRGLSGCMLCSQRRLSQQPVPERIPNRYLGQSPFTHPHLLRP 60  
  
 Qy 61 GEVTPGLSQVEYALRRHKLMSLIQKEAQGQSGTDQTVVVLNSNPTYYMSNDIPYTFHQDNN 120  
 |||||||  
 Db 61 GEVTPGLSQVEYALRRHKLMSLIQKEAQGQSGTDQTVVVLNSNPTYYMSNDIPYTFHQDNN 120  
  
 Qy 121 FLYLCGFQEPDSILVLQSLPGKQLPSHKAILFVPRRDPSRELWDGPRSGTDGAIALTGVD 180  
 |||||||  
 Db 121 FLYLCGFQEPDSILVLQSLPGKQLPSHKAILFVPRRDPSRELWDGPRSGTDGAIALTGVD 180  
  
 Qy 181 EAYTLEEFQHLLPKMKAETNMVWYDWMRPSHAQLHSDYMQPLTEAKAKSKNKVRGVQQLI 240  
 |||||||  
 Db 181 EAYTLEEFQHLLPKMKAETNMVWYDWMRPSHAQLHSDYMQPLTEAKAKSKNKVRGVQQLI 240  
  
 Qy 241 QRLRLIKSPAEIFERMQIAGKLTSQLAFIETMFTSKAPVVEAFLYAKFEFECCRARGADILAY 300  
 |||||||  
 Db 241 QRLRLIKSPAEIFERMQIAGKLTSQLAFIETMFTSKAPVVEAFLYAKFEFECCRARGADILAY 300  
  
 Qy 301 PPVVAGGNRSNTLHYVKNNQLIKDGEMLLDGGCESSCYVSDITRTWPVNGRFTAPQAEI 360  
 |||||||  
 Db 301 PPVVAGGNRSNTLHYVKNNQLIKDGEMLLDGGCESSCYASDITRTWPVNGRFTAPQAEI 360  
  
 Qy 361 YEAVLEIQRDCLALCFPGTSLENIYSMMLTLIGQKLKDLGIMKNIKENNAFKAAARKYCPH 420  
 |||||||  
 Db 361 YEAVLEIQRDCLALCFPGTSLENIYSMMLTLIGQKLKDLGIMKNIKENNAFKAAARKYCPH 420



Database : PIR\_79:\*

1: pir1:\*

2: pir2:\*

3: pir3:\*

4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Query					Description
	Score	Match	Length	DB	ID	
1	821.5	30.7	451	2	A86226	hypothetical prote
2	745	27.8	511	2	S50581	hypothetical prote
3	722.5	27.0	486	2	T37572	probable metallopr
4	712	26.6	444	2	H82992	aminopeptidase P P
5	709	26.5	436	2	AB1840	aminopeptidase P [
6	705.5	26.3	430	2	B64096	X-Pro aminopeptida
7	680.5	25.4	446	2	F82609	aminopeptidase P X
8	644	24.0	441	2	S76440	hypothetical prote
9	635.5	23.7	438	2	AH0873	proline aminopepti
10	623.5	23.3	441	2	C91101	proline aminopepti
11	623.5	23.3	441	2	G85946	proline aminopepti
12	614.5	22.9	441	1	DPECP	X-Pro aminopeptida
13	598	22.3	437	2	AG0111	X-Pro aminopeptida
14	534	19.9	383	2	F87719	protein R119.2 [im
15	473	17.6	491	1	JN0491	X-Pro aminopeptida
16	424.5	15.8	535	2	S56261	probable membrane
17	415	15.5	493	2	A32454	X-Pro dipeptidase

Database : Published\_Applications\_AA:\*

1: /cgn2\_6/ptodata/2/pubpaa/US07\_PUBCOMB.pep:\*

2: /cgn2\_6/ptodata/2/pubpaa/PCT\_NEW\_PUB.pep:\*

3: /cgn2\_6/ptodata/2/pubpaa/US06\_NEW\_PUB.pep:\*

4: /cgn2\_6/ptodata/2/pubpaa/US06\_PUBCOMB.pep:\*

5: /cgn2\_6/ptodata/2/pubpaa/US07\_NEW\_PUB.pep:\*

6: /cgn2\_6/ptodata/2/pubpaa/PCTUS\_PUBCOMB.pep:\*

7: /cgn2\_6/ptodata/2/pubpaa/US08\_NEW\_PUB.pep:\*

8: /cgn2\_6/ptodata/2/pubpaa/US08\_PUBCOMB.pep:\*

9: /cgn2\_6/ptodata/2/pubpaa/US09A\_PUBCOMB.pep:\*

10: /cgn2\_6/ptodata/2/pubpaa/US09B\_PUBCOMB.pep:\*

11: /cgn2\_6/ptodata/2/pubpaa/US09C\_PUBCOMB.pep:\*

12: /cgn2\_6/ptodata/2/pubpaa/US09\_NEW\_PUB.pep:\*

13: /cgn2\_6/ptodata/2/pubpaa/US10A\_PUBCOMB.pep:\*

14: /cgn2\_6/ptodata/2/pubpaa/US10B\_PUBCOMB.pep:\*

15: /cgn2\_6/ptodata/2/pubpaa/US10C\_PUBCOMB.pep:\*

16: /cgn2\_6/ptodata/2/pubpaa/US10D\_PUBCOMB.pep:\*

17: /cgn2\_6/ptodata/2/pubpaa/US10\_NEW\_PUB.pep:\*

18: /cgn2\_6/ptodata/2/pubpaa/US11\_NEW\_PUB.pep:\*

19: /cgn2\_6/ptodata/2/pubpaa/US60\_NEW\_PUB.pep:\*

20: /cgn2\_6/ptodata/2/pubpaa/US60\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result	Query					Description
	No.	Score	Match	Length	DB	
ID						
1	2680	100.0	507	9	US-09-780-016-2	Sequence 2, Appli
2	2680	100.0	507	14	US-10-214-811-2	Sequence 2, Appli
3	2680	100.0	507	16	US-10-766-074-2	Sequence 2, Appli
4	2657.5	99.2	532	9	US-09-780-016-20	Sequence 20, Appli
5	2657.5	99.2	532	14	US-10-214-811-20	Sequence 20, Appli
6	2657.5	99.2	532	16	US-10-766-074-20	Sequence 20, Appli
7	2558	95.4	484	9	US-09-780-016-26	Sequence 26, Appli
8	2558	95.4	484	14	US-10-214-811-26	Sequence 26, Appli
9	2558	95.4	484	16	US-10-766-074-26	Sequence 26, Appli
10	2535.5	94.6	509	9	US-09-780-016-24	Sequence 24, Appli
11	2535.5	94.6	509	14	US-10-214-811-24	Sequence 24, Appli
12	2535.5	94.6	509	16	US-10-766-074-24	Sequence 24, Appli

Database : Issued\_Patents\_AA:\*

1: /cgn2\_6/ptodata/1/iaa/5A\_COMB.pep:\*

2: /cgn2\_6/ptodata/1/iaa/5B\_COMB.pep:\*

3: /cgn2\_6/ptodata/1/iaa/6A\_COMB.pep:\*

4: /cgn2\_6/ptodata/1/iaa/6B\_COMB.pep:\*

5: /cgn2\_6/ptodata/1/iaa/PCTUS\_COMB.pep:\*

6: /cgn2\_6/ptodata/1/iaa/backfiles1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query			Description
		Match	Length	DB	
1	2680	100.0	507	4	US-09-780-016-2
2	2680	100.0	507	4	US-10-214-811-2
3	2657.5	99.2	532	4	US-09-780-016-20
4	2657.5	99.2	532	4	US-10-214-811-20
5	2558	95.4	484	4	US-09-780-016-26
6	2558	95.4	484	4	US-10-214-811-26
7	2535.5	94.6	509	4	US-09-780-016-24
8	2535.5	94.6	509	4	US-10-214-811-24
9	2255	84.1	428	4	US-09-780-016-22
10	2255	84.1	428	4	US-10-214-811-22

Database : A\_Geneseq\_23Sep04:\*

1: geneseqp1980s:\*

2: geneseqp1990s:\*

3: geneseqp2000s:\*

4: geneseqp2001s:\*

5: geneseqp2002s:\*

6: geneseqp2003as:\*

7: geneseqp2003bs:\*

8: geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	Query					Description
No.	Score	Match	Length	DB	ID	
1	2680	100.0	507	4	AAE06717	Aae06717 Human nov
2	2657.5	99.2	532	4	AAE06726	Aae06726 Human nov
3	2558	95.4	484	4	AAE06729	Aae06729 Human nov
4	2535.5	94.6	509	4	AAE06728	Aae06728 Human nov
5	2532.5	94.5	515	7	ADE72525	Ade72525 Human end
6	2532.5	94.5	515	7	ADE72526	Ade72526 Human end
7	2255	84.1	428	4	AAE06727	Aae06727 Human nov
8	2255	84.1	428	5	ABP43879	Abp43879 Human pro
9	2232.5	83.3	453	4	AAE06725	Aae06725 Human nov
10	2126	79.3	408	4	AAM06839	Aam06839 Human foe
11	1887	70.4	371	8	ADJ71985	Adj71985 Human PMM
12	1494.5	55.8	298	4	ABG22568	Abg22568 Novel hum